

a1 filled in bars below the sequences NVSS and NFSV represent potential N-glycosylation sites.

Replace the paragraph on page 2, lines 17-21 with the following new paragraph:

a2 Figure 5 shows a representation of the amino acid sequence of the TIG-1 protein: The glutamine and serine/proline rich domains are noted. The glutamine rich repeat sequences are shown (SEQ ID NO: 6). The putative nuclear localization signal is shown in black.

Replace the paragraph on page 15, lines 25-31 with the following new paragraph:

sub B2  
a3 An example of the protein is the protein encoded by the nucleotide sequence as shown in SEQ ID NO:1 (this is the open reading frame). The amino acid sequence encoded by this nucleotide sequence is shown in SEQ ID NO:3. The full nucleotide sequence is as shown in SEQ ID NO:2.

Replace the paragraph on page 30, lines 14-25 with the following new paragraph:

a4 The protocol elaborated by Wang and Brown 1991 with some modification. Long cDNAs were digested with the restriction endonuclease Rsa 1 and then ligated to linker DNAs (SEQ ID NO:7: 5'GAATTCAGATCTCCCGGGTCACCGC3' and SEQ ID NO:8: 5'TGACCCGGGAGATCGAATTC3'). Linkered cDNA fragments were amplified by PCR. PCR amplified cDNA fragments constructed from the TPA induced mRNAs were used as "tracer" cDNAs, while a five fold molar excess of biotinylated PCR amplified cDNA fragments constructed from hemin induced mRNAs were used as "driver" cDNAs to produce a EST library that was highly enriched in cDNA fragments generated from the TPA induced K562 cells.

After the Abstract:

Delete the originally filed SEQUENCE LISTING pages 1-3.  
Add new SEQUENCE LISTING pages 1-7, enclosed herewith.